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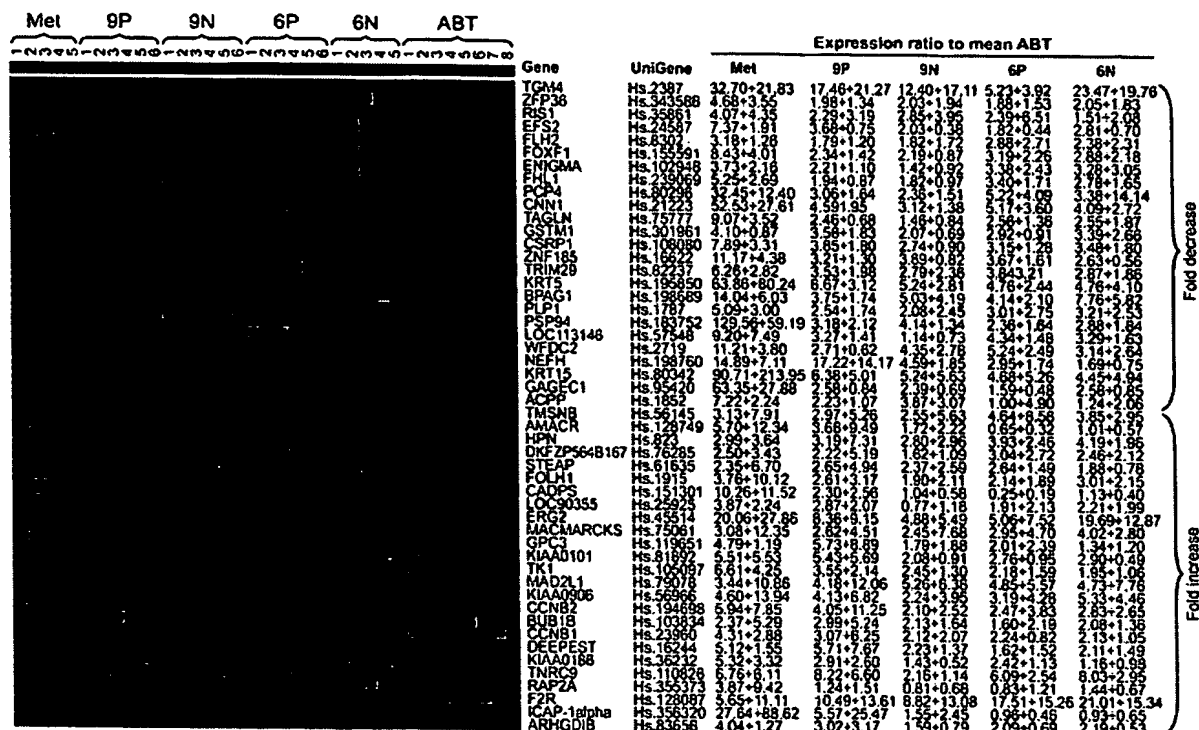


Fig. 1

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Gene	Primers and Probe		Amplicon bp
ZNF185	FP	TGG ATG AAA GGC AAG GTA AAG AG	84
	RP	TTC TAA AAC TCC CTT AAA GGC AGA CT	
	Probe	CCA AGA TAG GCT GGC TTC CCC CG	
PSP94	FP	AGT GAA TGG ATA ATC TAG TGT GCT TCT AGT	100
	RP	GCA TGG CTA CAC AAT CAT TGA CTA T	
	Probe	CCC AGG CCA GGC CTC ATT CTC CT	
BPAG1	FP	TCG CTG AAA GAG CAC GTC AT	94
	RP	AGC AAT CTA AAA CAC TGC AGC TTG	
	Probe	AAT CAA AGA GAA AGA TAT AAA TTC GTT CCC ACA GCC	
Erg-2	FP	TCC TGT CGG ACA GCT CCA AC	75
	RP	CGG GAT CCG TCA TCT TGA	
	Probe	TGC ATC ACC TGG GAA GGC ACC AAC	

Fig. 2a

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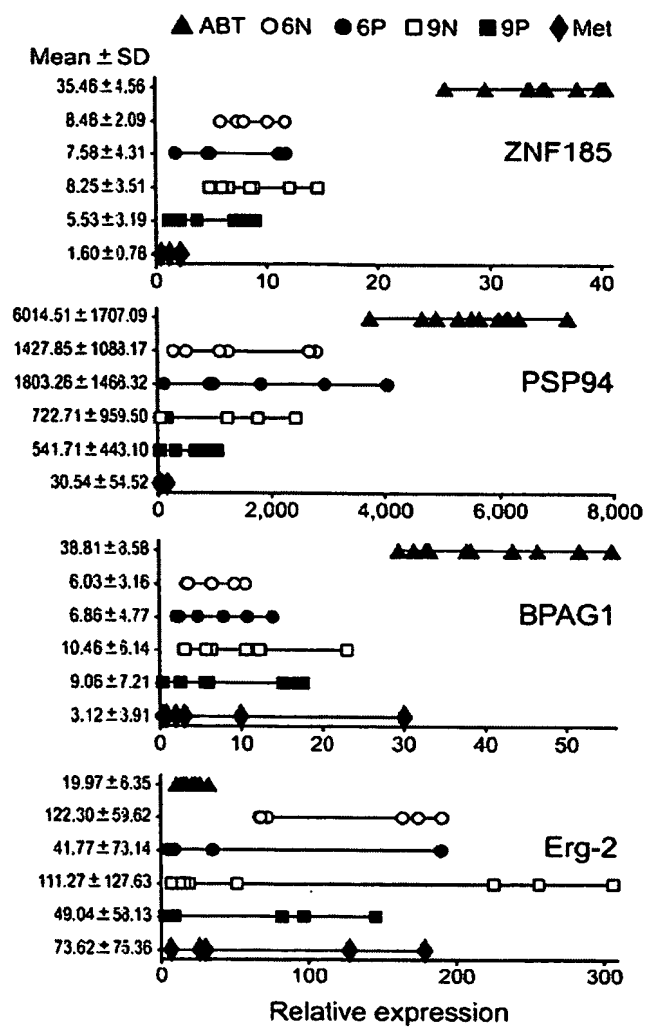


Fig. 2b

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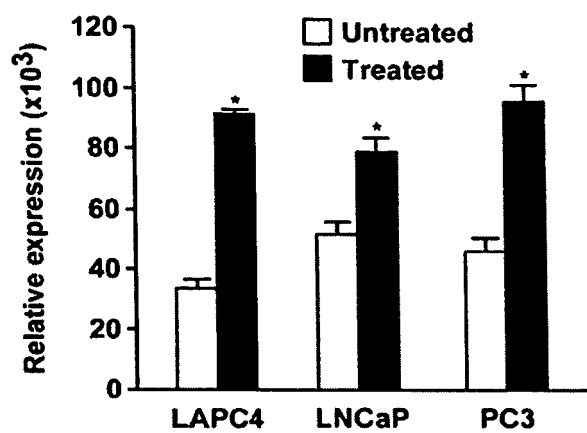


Fig. 3a

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Primer set			Size (bp)	Genomic position
1 W	FP	GCGCAGTTCGGGTG TCTGTC	197	210
	RP	GCGGGGAGGACCAGCGTTAG		
1 M	FP	GCGTAGTTTCGGGTG TTTG	197	210
	RP	ACGAAAAAAACCAAC TTA ACTA		
1 U	FP	G TGTAGTTTIGGGTG TTTGTTAGG	198	210
	RP	C AAAAAAAACCAAC TTA ACTATTCTC		
2 W	FP	CCTGGGACTCCGTCA GACTGG	148	335
	RP	GACAGACACCCGGA ACTGCG		
2 M	FP	T TGGGATTTGTTAGATTGG	145	335
	RP	AACAAACACCCGAA ACTACG		
2 U	FP	TGGGATTTTGT TAGATTGGAAAGG	146	333
	RP	CTAACAAACACCC A AACTACACCA		

Fig. 3b

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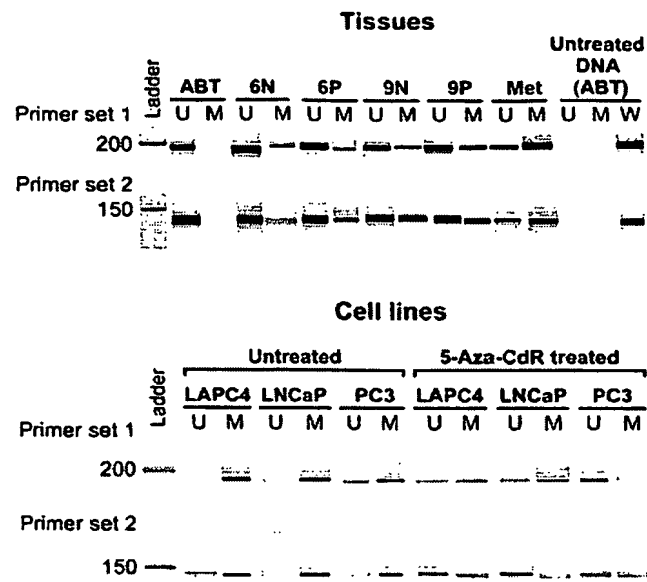


Fig. 3c

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Samples	Total	Methylated (%)
Benign prostatic tissues	12	0 (0)
Gleason Score 6 tumors	11	4 (36.3)
Gleason Score 9 tumors	14	7 (50)
Metastatic tissues	5	5 (100)

Fig. 3d

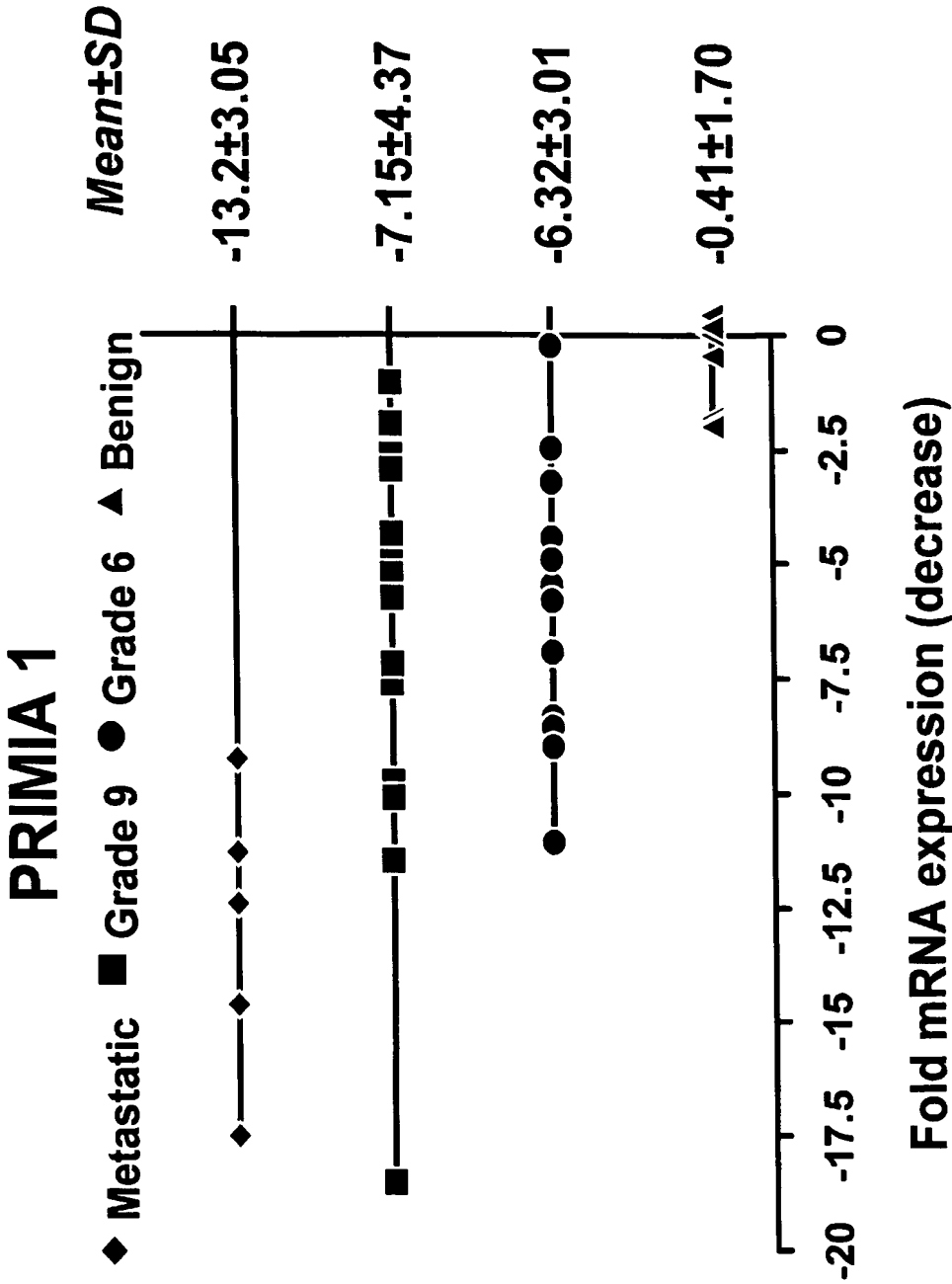
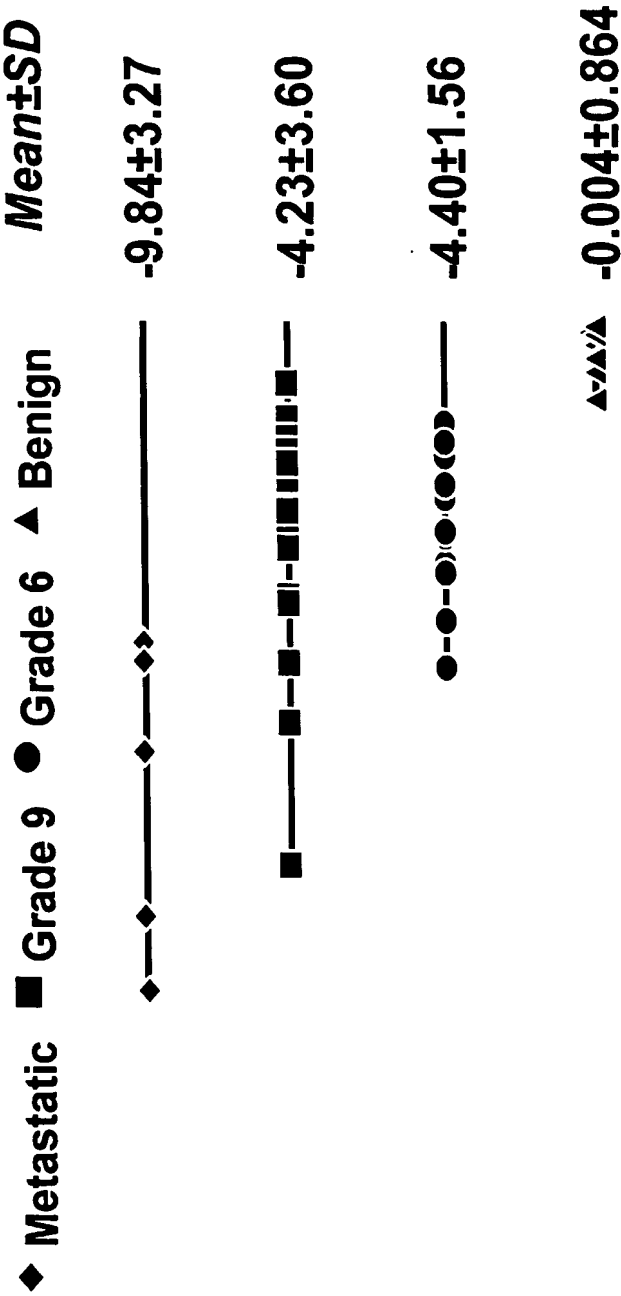


Fig. 4



Fold mRNA expression (decrease)

Fig. 5

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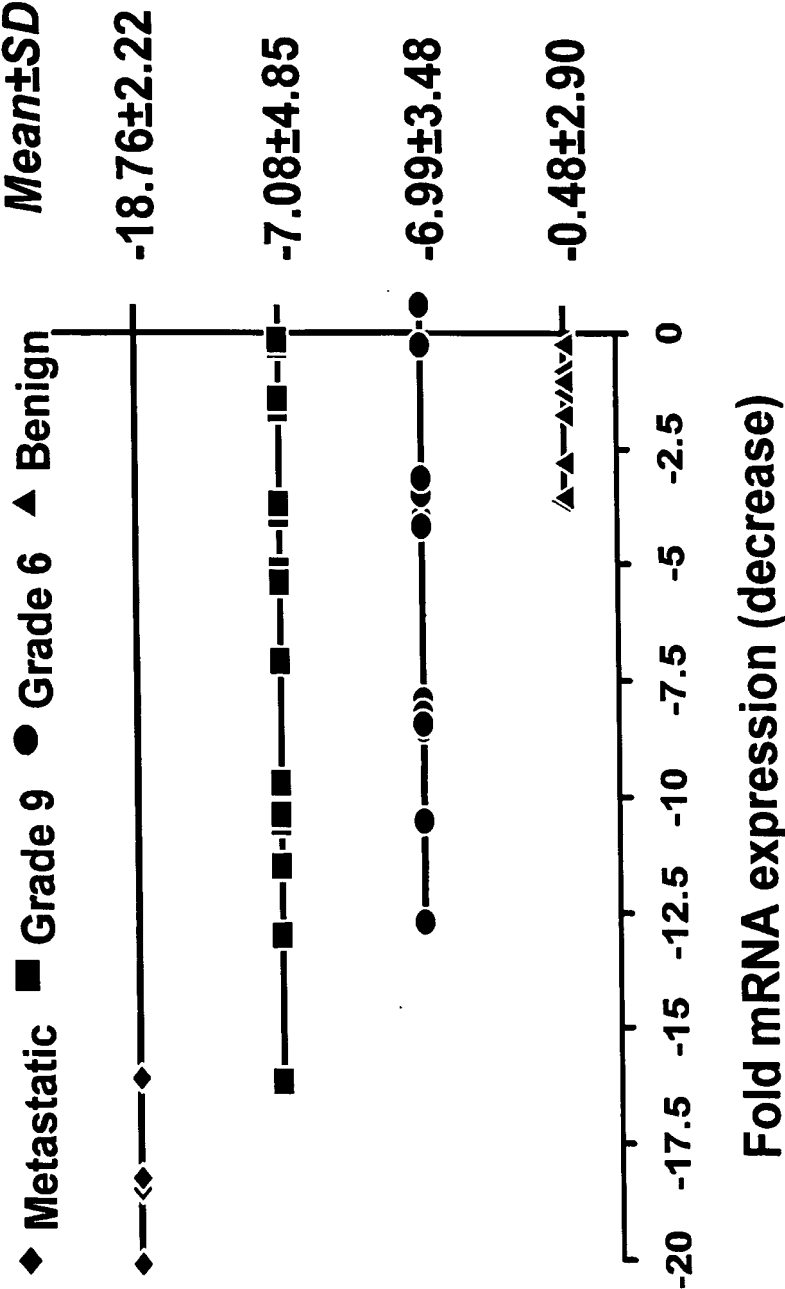


Fig. 6

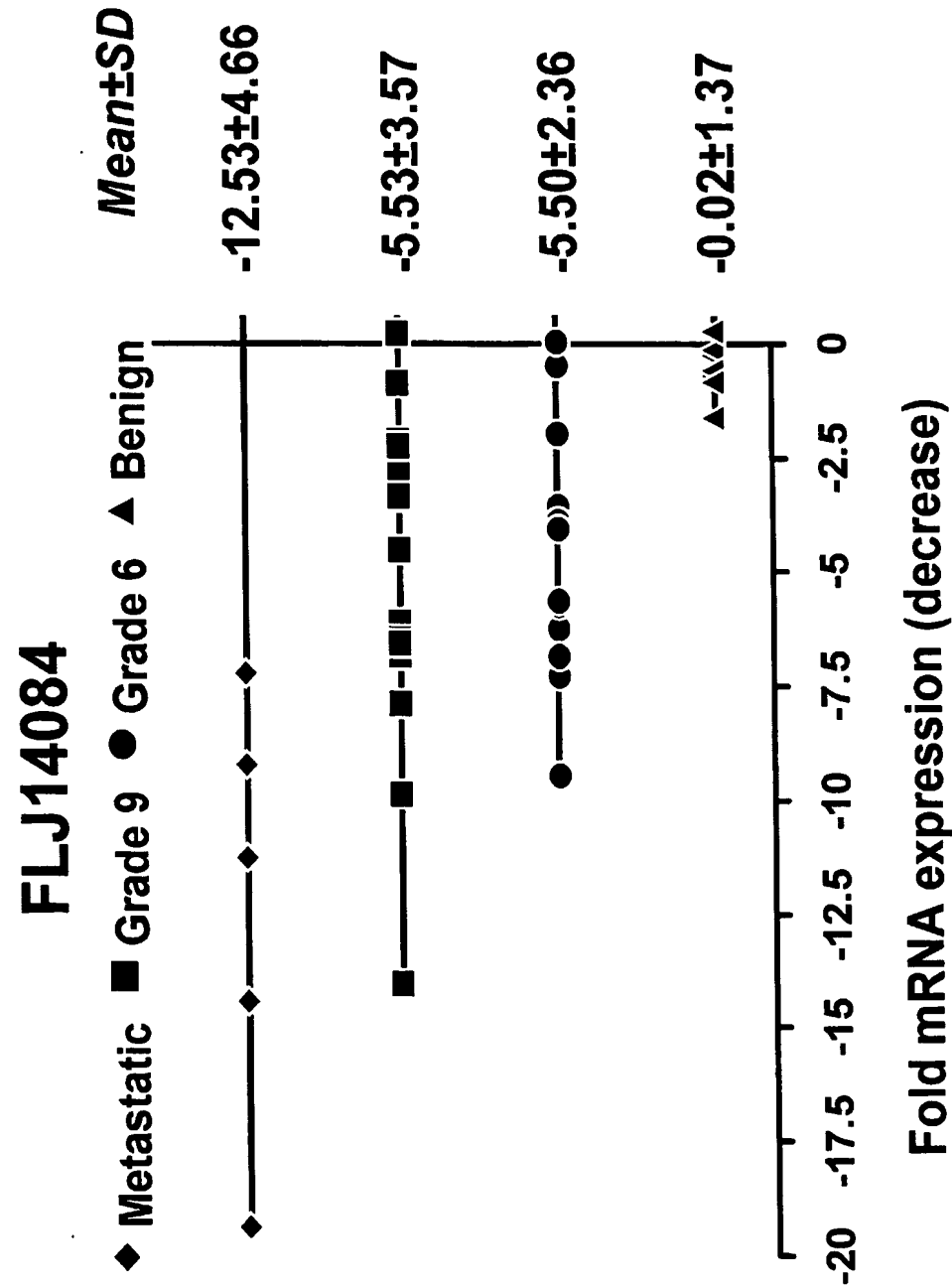
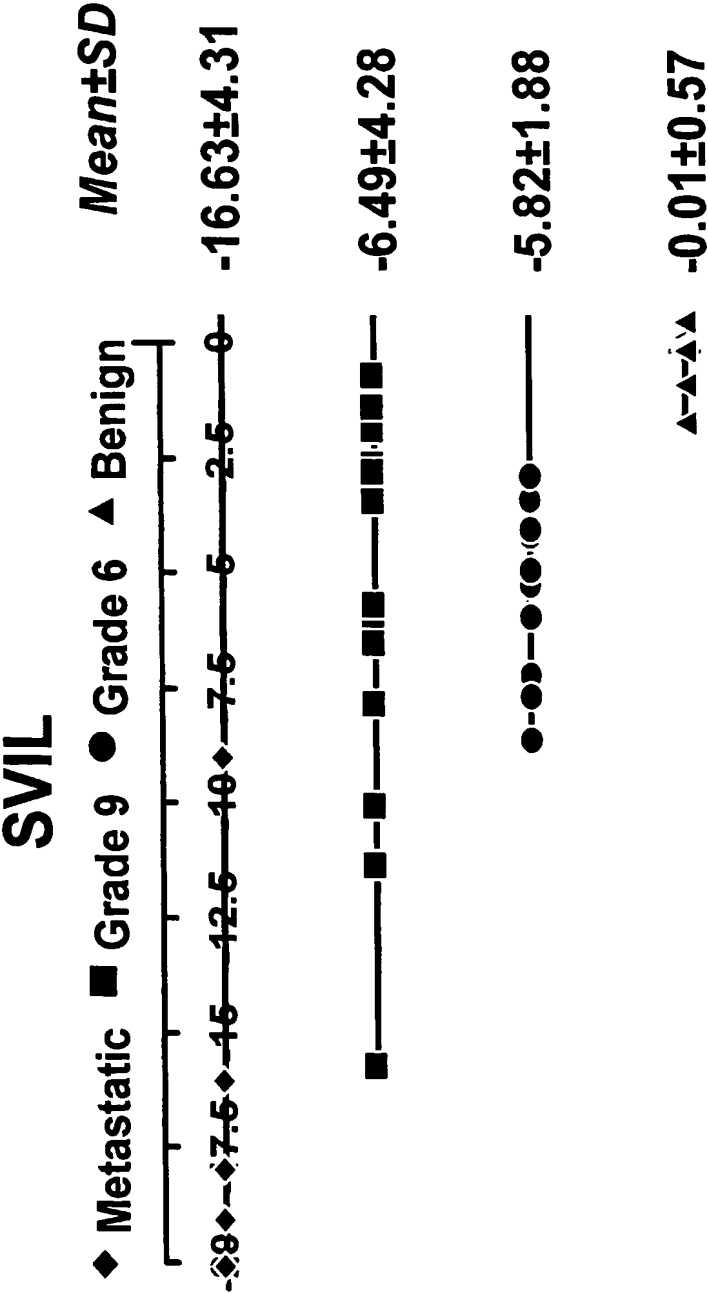


Fig. 7



Fold mRNA expression (decrease)

Fig. 8

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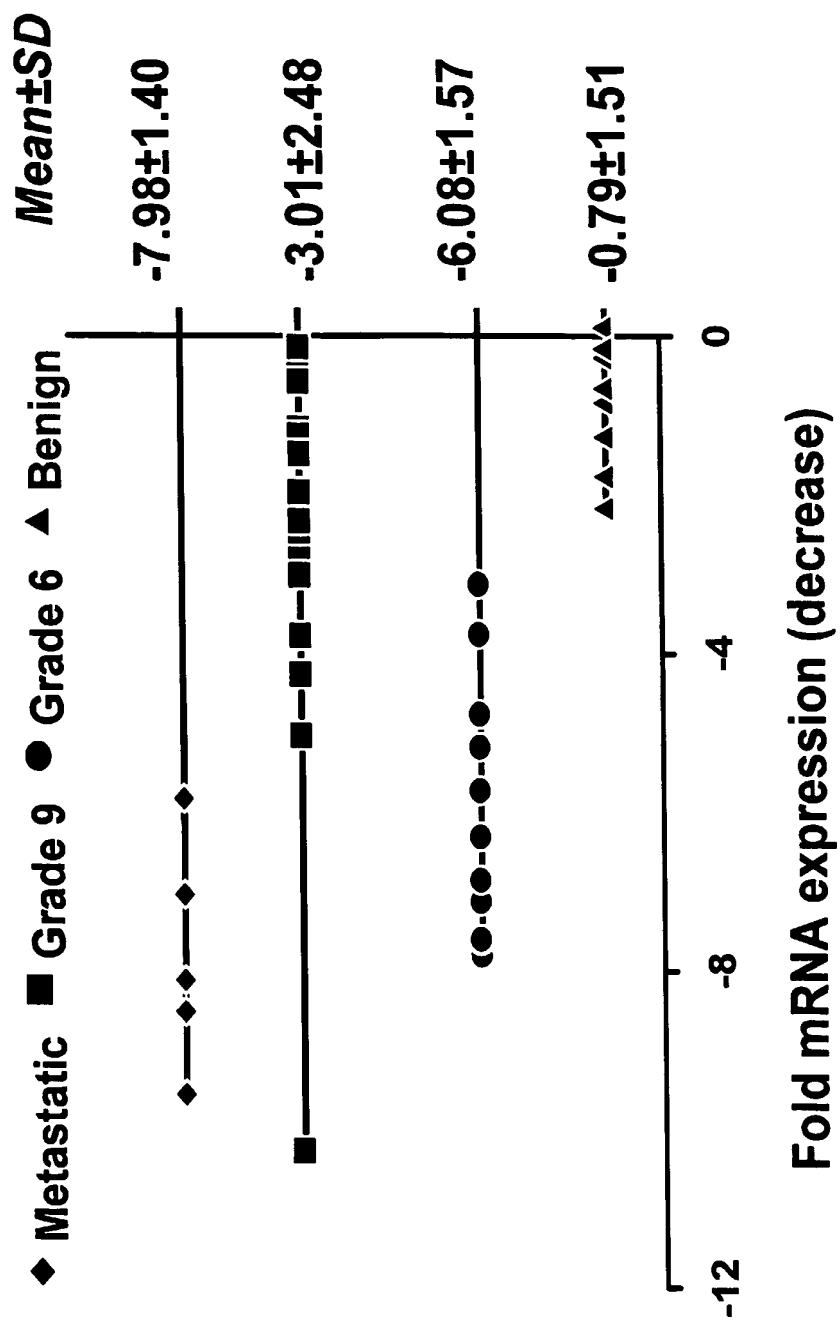


Fig. 9

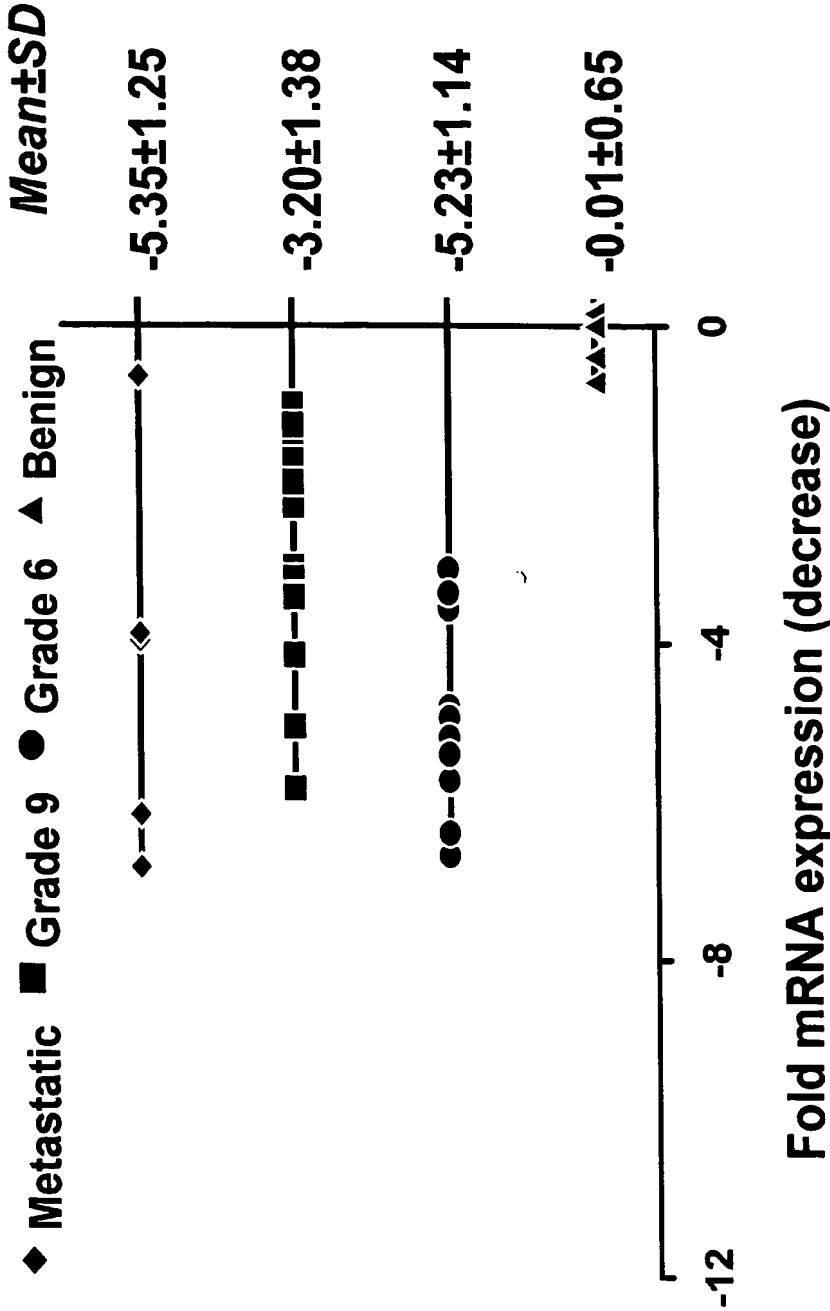


Fig. 10

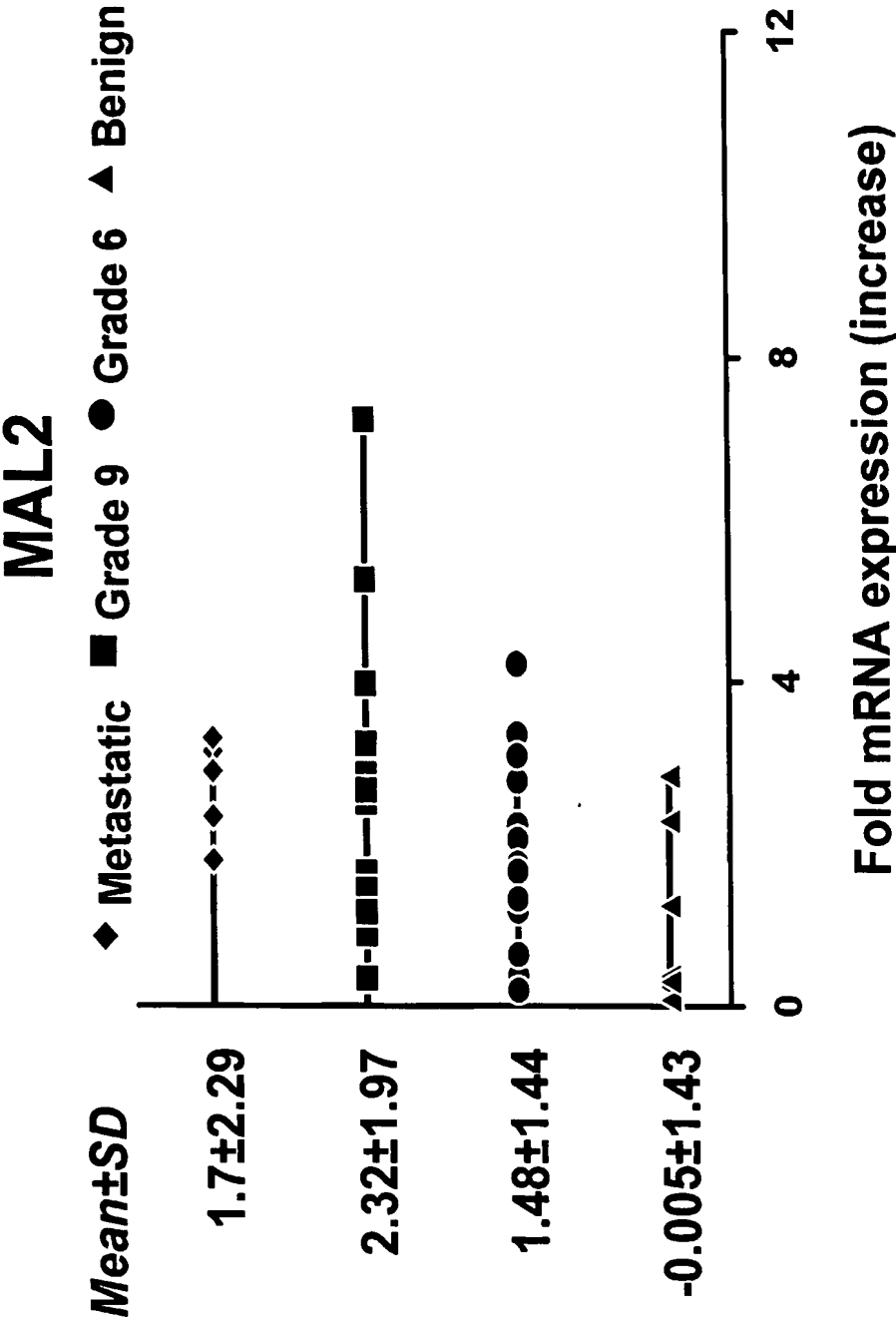


Fig. 11

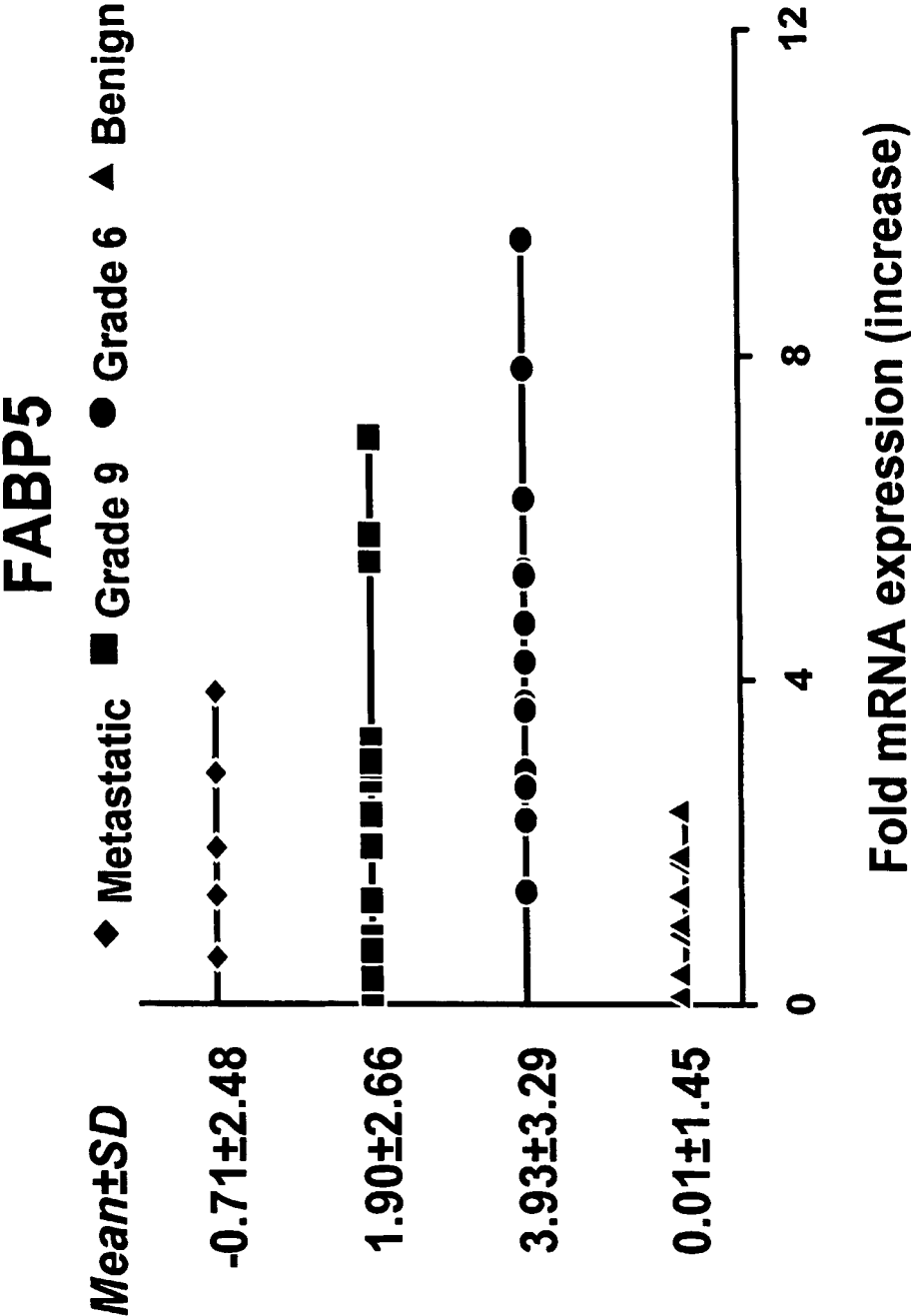


Fig. 12

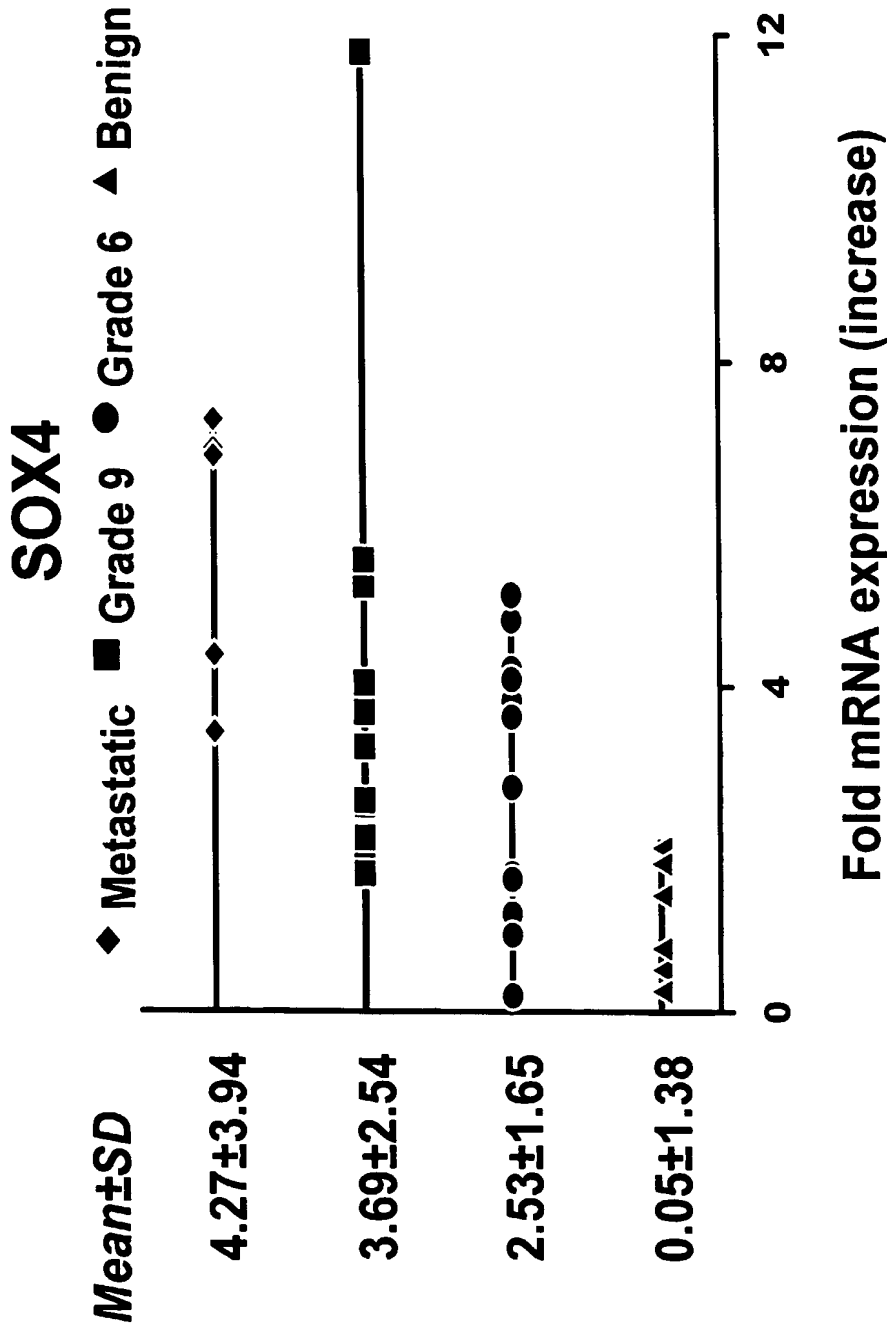


Fig. 13

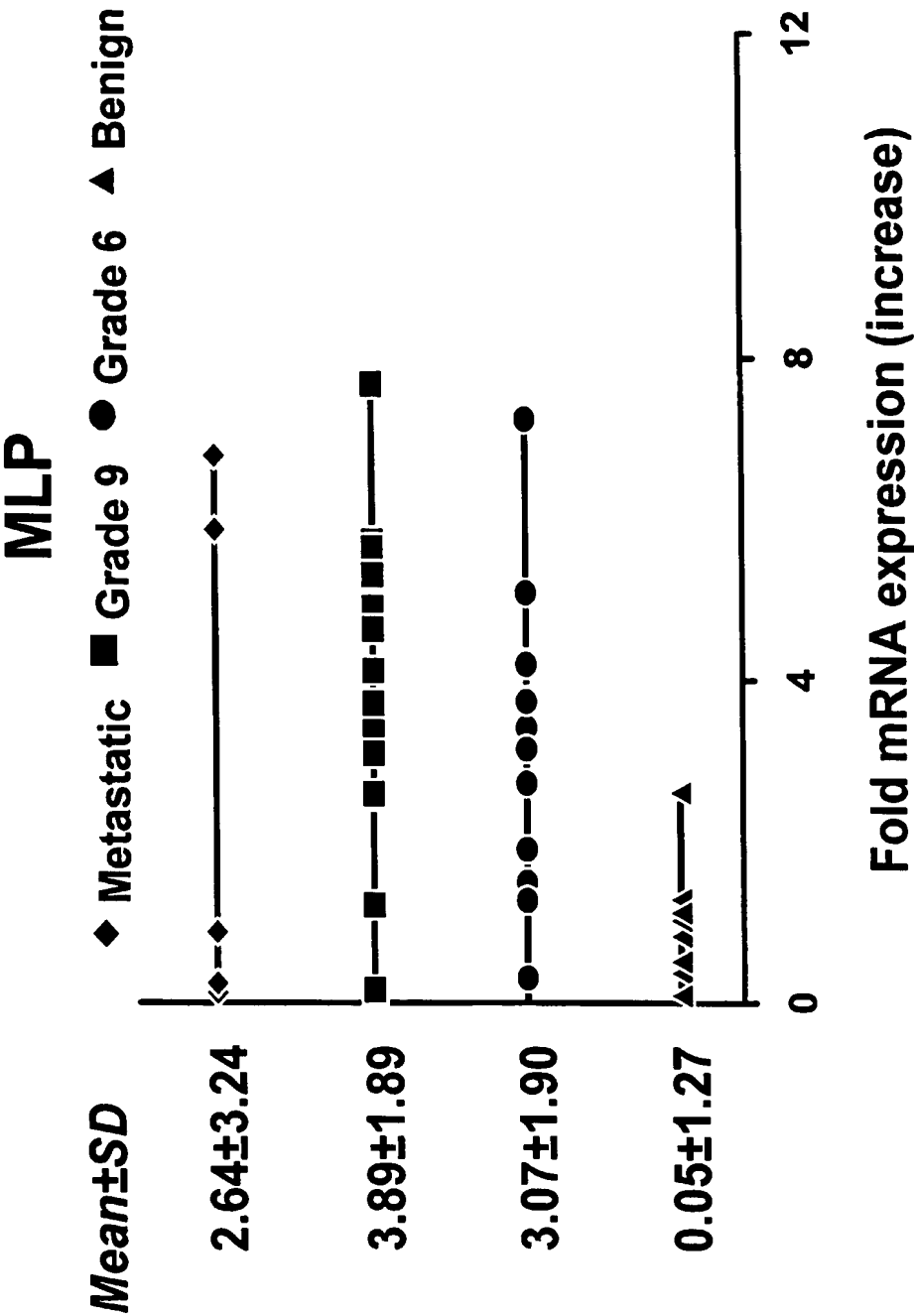


Fig. 14

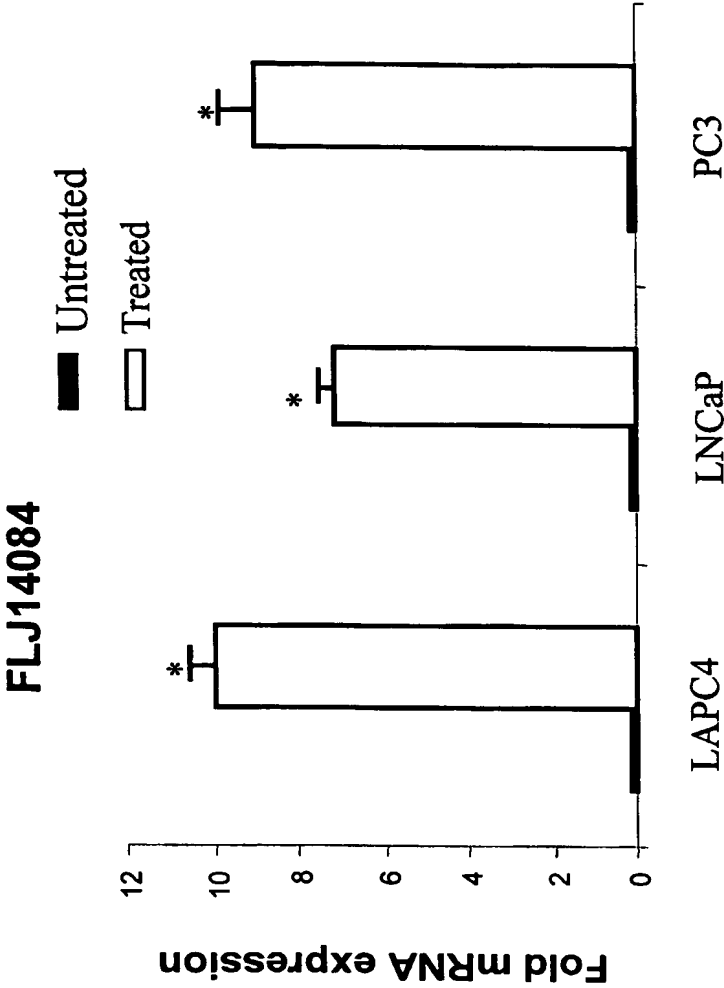


Fig. 15

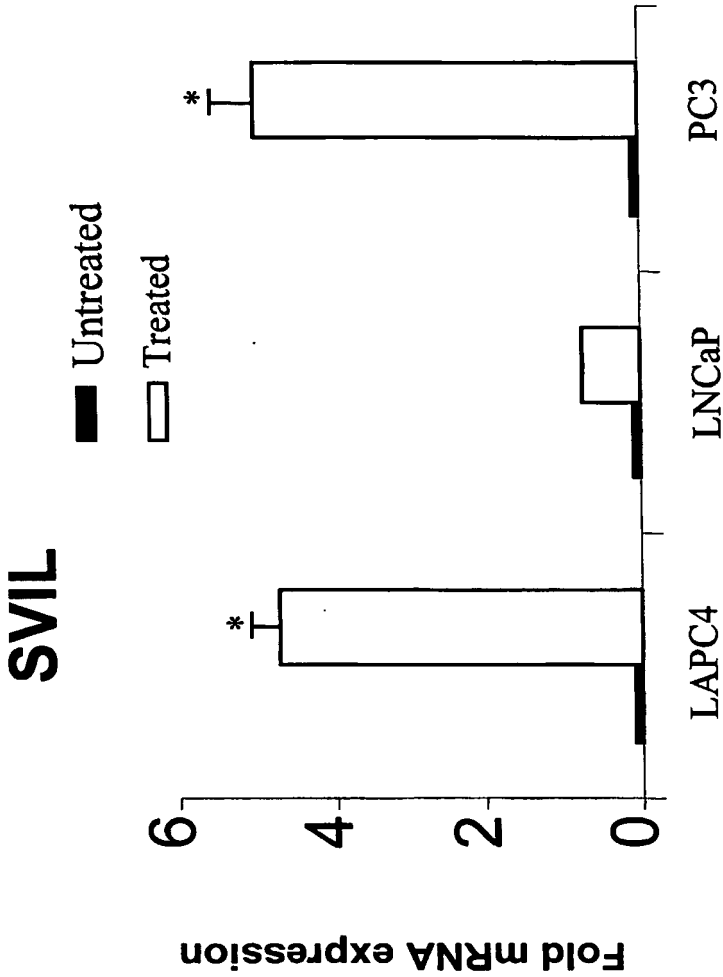


Fig. 16

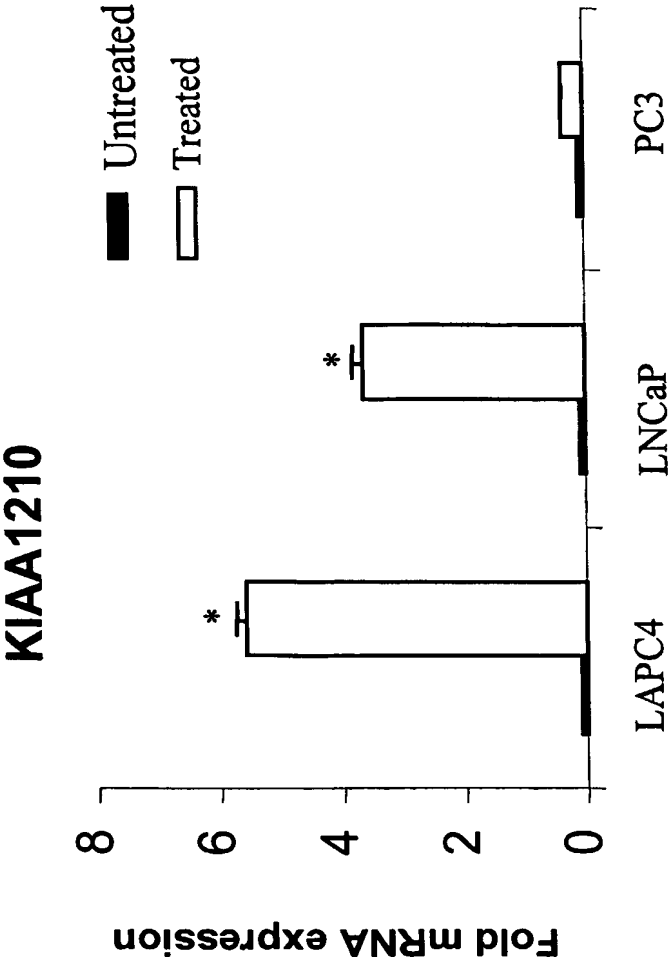


Fig. 17

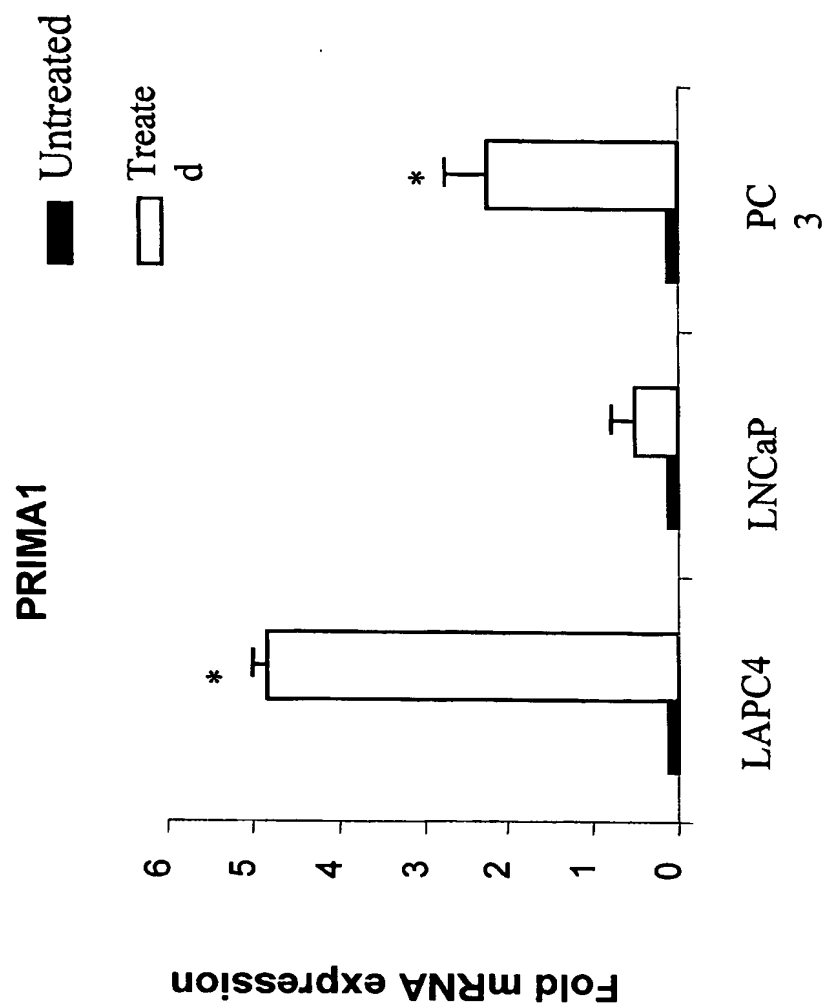


Fig. 18

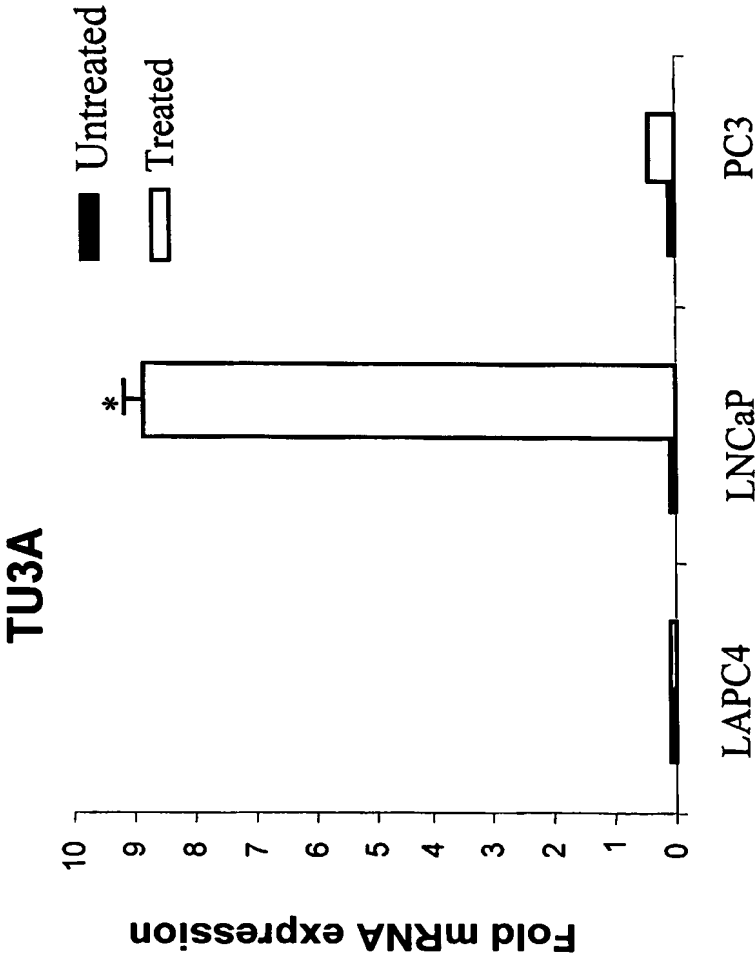


Fig. 19